

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGC
 GAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACGCGTCCTCAGGGACGACTCTGCCATC
 GAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAG
 AAAAGTTCTCGGCAGGTCTGTGGAGGTCTGGGTCTCTACTTCACGCACCCGAGGACGTTCCGGCAATC
 CGCGACAAAATAAGGAAGCACCCCGCGGTTCATCGACATCTACGAGTACGACATACCCCTTCGCCAAGCGCTAC
 CTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCTTCGACATCGAGACG
 CTCTACCACGAGGGAGAAGAGTTTGAACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCG
 CGCGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAG
 CGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGAGCTGTGATAACATAACCGCGACAACCTTCGACTTC
 GCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACCCCTCGGGAGGGACGGGAGCGAGCCGAAG
 ATACAGCGCATGGGGGACAGGTTTGGCGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATA
 AGGCGCACCATAAACCTCCCGACCTACACCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAG
 AAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCG
 ATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCAGGCTC
 ATCGGCCAAGGCCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCTTAAGGAAG
 GCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTAC
 gcCGGTGGCTACGTCAAGGAGCCGAGCGGGGACTGTGGGACAATATCGTGATCTAGACTTTCGTAGTCTC
 TACCTTCAATCATAATCACCCACAACGTCTCGCCAGATACGCTCAACCGCGAGGGGTGTAGGAGTACGAC
 GTTGCCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTTCAATCCGAGCCTGTCTCGAAACCTG
 CTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGAT
 TACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCAGGGCAAGATGG
 TACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGCTT
 GAGGAAAAGTTCGGTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCTTGAGCGGAC
 GCTGAAACAGTCAAGAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAAGTCCCCGGCCTTCTCGAA
 CTGGAATACGAGGGCTTCTACGTACAGGGGCTTCTTCGTACGGAAGAAAAGTACCGGGTCATCGACGAGGAG
 GGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGGACTGGAGCGAGATAGCGAAGGAGACGCAGGCG
 AGGGTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCGTCAGAATTGTCAGGGAAGTCACCGAA
 AAGCTGAGCAAGTACGAGGTTCCGCCGAGAAGCTGGTTATCCACGAGCAGATAACCGCGGAGCTCAAGGAC
 TACAAGGCCACCGCCCGCACGTAGCCATAGCGAAgcGTTTGGCCGCCAGAGGTGTTAAATCCGGCCCGGA
 ACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTC
 GACCCGACGAAGCACAACTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGCGAGTTGAGAGAATC
 CTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTGGGGCTTGGCGCGTGG
 CTGAAGCCGAAGGGGAAGAAGAAGTGA

FIG. 1

MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVRAEKVK
KKFLGRSVEVWVLYFTHPQDVPARDKIRKHPAVIDIYEDIPFAKRYLIDKGLIPMEGEEELKMSFDIET
LYHEGEEFGTGPILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDLITYNGDNFDF
AYLKKRCEKLGVSFTLGRDGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKE
KVYAEIATAWETGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRK
AYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYD
VAPEVGHKFKCDFPGFIPSLGNLLEERQKIKRKMATLDPLEKNLLDYRQRAIKILANSYGYGYARARW
YCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLE
LEYEGFYVRGFFVTKKKYAVIDEKGITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTE
KLSKYEVPPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYIVLKGSGRIGDRAIPFDEF
DPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

FIG. 2

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSAIEE
 IKKITAERHGRVVKVKRAEKVKKKFLGRSVEVWVLYFTHPQDVPAlRDKI
 RKHPAVIDIYEDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGE
 EFGTGPILMISYADESEARVITWKKIDLPYVEVVSSTEKEMIKRFLRVVKE
 KDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGRDGSEPQIQRMGDRFAV Extein 1
 EVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEElATAWE
 TGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSSTG
 NLVEWFLLRKAYERNELAPNKPDERELARRRGYAGGYVKEPERGLWDNI
 VYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFKCKDFPGFIP
 SLLGNLLEERQKIKRKMkatLDPLEKNLLDYRQRAIKILAN

SLLPGEWVA
 VIEGGKLRPVRIgELVDGLMEASGERVKRDGDTEVLEVEGLYASPSTGSP
 RKPAQCR*KP**GTAMPGKFTE*LSTPEGGLSVTRGHSLFAYRDASLWR*
 RGRRRFKPGDLLAVPSG*PSRRGGRGSTSLNCSSNCPRRKRPTCHRHSgK
 GRKNFFRGMLRTLrWIFGEEKTGGRPGATWSTLRGLGYVKLRKIGYGVVD
 REGLGKVPRFYERLVEVIRYNGNRGEFIADFNALRPVLRlMMPEKELEEW Intein 1
 LVGTRNGFRIRPFIEVDWKFAKLLGYVVSSEGsAGKWKNRtGGWSYSVRLY
 NEDGSVLDDMERLARSSLGA*ARGELRRDFKEDGLHNLRGALRFTGREQE
 GSVAYLHVP*GGPLGLP*GVLHRRRRRSPEQDGSALHQERASG*RPRPAP
 ELAGRLSDKRPPRQRLQGLRERGtALYRVPEAEERLTYSHVIPREVLEE
 TSAGPSRRT*VTGNSGSWWKAGSSTRKGPVG*AGSSTGI*SSTGSRKSGR
 KATRGTSTT*ALRRTRTSgGLWVPLRAQX

SYYGYYGYARARWYCRECAES
 VTAWGReYIEMVIRELEEKFGFKVLYADTDGLHATIPGADAETVKKKAME
 FLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVR
 RDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKLVI Extein 2
 HEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYIVLKGSGRIGD
 RAIPFDEFDPtKHKYDADYYIENQVLPaverILRAFGYRKEDLRYQKTRQ
 VGLGAWLKPKGKKK

FIG. 3

AATTCCACTGCCGTGTTTAACTTTCCACCGTTGAACTTGAGGGTGATTT
 TCTGAGCCTCCTCAATCACTTAATCGAGACCGCGGATTACCTTGAACGG
 TACACGTTCAACGATTCGGTTCCTGTAATGGTCGATACTGGGCCGTGCTG
 GATTTTCTAAACGTCTCAAGAACGGCTTTTCATCAACGGAACTGCCACGT 5' untranslated sequence
 CTCCGCCGTGTCGAGGGTTAAACCTGAAGTTCAAGACTTTGCAACGGAAT
 GCGGAGAGAACGGCGACTACCCAGTGAAGAGCTTTTGAAGCCAAAGC
 CGAGCTTCAGCGAATGTGCGGTGCCCTTGTTCAAGAGTTGTGAGCCCTTG
 ATTGTTGTTTTCTCCTCTTTTCTGATAACATCGATGGCGAAGTTATTAG
 TTCTCAGTTCGATAATCAGGCAGGTGTTGGTC

ATGATCCTTGACGTTGAT
 TACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAA
 CGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACG
 CGTCTCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCG
 GAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAA
 AAAGTTCCTCGGCAGGTCTGTGGAGGTCTGGGTCTCTACTTCACGCACC
 CGCAGGACGTTCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGGTG
 ATCGACATCTACGAGTACGACATACCCTTCGCCAAGCGCTACCTCATAGA
 CAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCCT
 TCGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGAACCGGGCCG
 ATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGGTGATAACCTG
 GAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGA
 TGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTG
 ATAACATACAACGGCGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTG
 TGAGAAGCTTGGCGTGAGCTTTACCTCGGGAGGGACGGGAGCGAGCCGA Extein 1
 AGATACAGCGCATGGGGGACAGGTTTGCGGTGAGGTGAAGGGCAGGGTA
 CACTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCCGACCTA
 CACCCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGG
 TCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGGCTTGAG
 AGGGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGG
 CAGGGAGTTCTTCCCGATGGAGGCCAGCTTTCCAGGCTCATCGGCCAAG
 GCCTCTGGGACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTC
 CTCTTAAGGAAGGCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCCGA
 CGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTACGCCGGTGGCTACGTCA
 AGGAGCCCGAGCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGT
 AGTCTCTACCTTCAATCATAATCACCCACAACGTCTCGCCAGATACGCT
 CAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCGAGGTCGGTCACA
 AGTTCCTGCAAGGACTTCCCGGCTTCATTCCGAGCCTGCTCGGAAACCTG
 CTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCC
 GCTGGAGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTCTCG
 CCAAC

FIG. 4

AGCCTTCTTCCCGGGAGTGGGTTGCGGTCATTGAAGGGGGGAAA
 CTCAGGCCCGTCCGCATCGGCGAGCTGGTTGATGGACTGATGGAAGCCAG
 CGGGGAGAGGGTGAAAAGAGACGGCGACACCGAGGTCTTTGAAGTCGAGG
 GGCTTTACGCCTCTCCTTCGACAGGGAGTCCAAGAAAGCCCGCACAATGC
 CGGTGAAAGCCGTGATAAGGCACCGCTATGCCGGGAAGTTTACAGAATA
 GCTCTCAACTCCGGAAGGAGGATTAAGCGTGACGCGCGGCCACAGCCTCT
 TCGCGTACCGGGACGCGAGCTTGTGGAGGTGACGGGGGAGGAGGAGGTTT
 AAGCCCGGCGACCTCCTGGCGGTGCCAAGCGGATAACCCTCCCGGAGAGG
 AGGGAGAGGCTCAACATCGTTGAACTGCTCCTCGAACTGCCCGAGGAGGA
 AACGGCCGACATGTCATCGACATTCCGGCAAGGGTAGAAAGAACTTCTTC
 AGGGGAATGCTCAGAACCTCCGCTGGATTTTCGGGAGGAGAAGACCGG Intein 1
 AGGGCGGCCAGGCGCTACCTGGAGCACCTTGCCTGGGCTCGGCTACGTGA
 AGCTGAGGAAAATCGGCTACGGGCTGGTTGATAGGAGGGACTGGGAAAG
 GTACCGCGCTTCTACGAGAGGCTCGTGGAGGTAATCCGCTACAACGGCAA
 CAGGGGGGAGTTCATCGCCGATTTC AACGCGCTCCGCCCCGTCTCCGCC
 TGATGATGCCCGAGAAGGAGCTTGAAGAGTGGCTCGTTGGGACGAGGAAC
 GGGTTTCAGGATAAGGCCGTTTCATAGAGGTTGATTGGAAGTTTCGAAAGCT
 CCTCGGCTACTACGTGAGCGAGGGGAGCGCCGGGAAGTGGA AAAACCGGA
 CCGGGGGCTGGAGCTACTCGGTGAGGCTTTACAACGAGGACGGGAGCGTT
 CTCGACGACATGGAGAGACTCGCGAGGAGTTCTTTGGGGCGTGAGCGCG
 GGGGGAAC TACGTCGAGATTTCAAAGAAGATGGCCTACATAATCTTCGAG
 GGGCTCTGCGGTTACCGGCCGAGAACAAGAGGGTTCCGTGGCTTATCTT
 CACGTCCCTGAGGAGGTCCGCTGGGCCTTCCTTGAGGGGTACTTCATCG
 GCGACGGCGACGTTCACCCGAGCAAGATGGTTCCGGCTCTCCACCAAGAGC
 GAGCTTCTGGCTAACGGCCTCGTCCTGCTCCTGAACTCGCTGGGCGTCTC
 AGCGATAAACGTCCGCCACGACAGCGGGGTTTACAGGGTCTACGTGAACG
 AGGAACTGCCCTTTACAGAGTACCGGAAGCGGAAGAACGCCTCACTTACT
 CCCACGTCATACCGAGGGAAGTGCTGGAGGAGACTTCGGCCGGGCCTTCC
 AGAAGAACATGAGTCACGGGAAATTCAGGGAGCTGGTGAAAGCGGGGAG
 CTCGACGCGGAAAGGGCCGTTAGGATAGGCTGGCTCCTCGACGGGGATAT
 AGTCCTCGACAGGGTCTCGGAAGTCAGGAAGGAAAGCTACGAGGGGTACG
 TCTACGACCTGAGCGTTGAGGAGGACGAGAACTTCTGGCGGGCTTTGGGT
 TCCTCTACGCGCACAACNN

FIG. 4 (cont.)

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AGCTACTACGGCTACTACGGCTATGCCAGGG
CAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGG
GAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAAAGTTCGGTTTAA
AGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCCTGGAGCGG
ACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTCTTAAACTATATCAAT
CCCAAACGCGCCGGCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAG
GGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGAGGGCA
AGATAACCACGCGCGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATA
GCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGA Extein 2
CGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCA
AGTACGAGGTTCGCGCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGC
GAGCTCAAGGACTACAAGGCCACCGGCCGACGTAGCCATAGCGAAGCG
TTTGGCCGCCAGAGGTGTAAAAATCCGGCCCGAACTGTGATAAGCTACA
TCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGAC

GAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAA
CCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCA
AGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTGGGGCTTGGCGCGTGG
CTGAAGCCGAAGGGGAAGAAGAAGTGA

GGAATTATCTGGTTTCTTTTCCC
AGCATTAATGCTTCCGACATTGCCTTATTTATGAAATCCTGTTGTGCC
TGAGTTTGTGCCAGAAAACAGCCTGTTCTGACGGCGCTTTTCTTGCCAG
GTCTCTTGAGTTTCGCAAGGGTCTTCTCGACCAGCTCAATGGTCTTGTCG
TCATTGTTTNNNNNNNNNNNNNNNNNNNNCCGGGGACTTCATACTGGC
GGTAATAGACAGGGATTCCCTTCCTCAAGGACTTCCCGGAGGCATTGGAG
TTTTTTGGTGGGGCTTTCACAGGATTTGCTCATCTTGTTGGATTTCTCGTT
CGATTGAATCTGTCCACTTGAGGGTGTAGGTCGAGACGGTGGAGCGCGTA
TTCCGGGAGCGGGTCTTGAGGCTCCATTTTTCAGTCCCTCCGGCGAAG 3' Untranslated sequence
AAGTGAACTCAAGCCGGGTGTTAGCTTATGTTATGTTCCCAACTCCTCC
AGCACCTCCAGGATCCCTCAATCCCGGAACCTCGAAGCCCTCTCGTGG
ATCTTTCTAACTTCCTCTGCCTCCGGGTTTATCCAGACCGCCACATGCC
GGCTCTCAGCGCACCTCGAAATCCTCCGCGTAGGTGTCGCCGATGTGGA
TTGCCCTCGTCCGGCTCGACCCCGAAGCATCGAGCGGTTTTCTGAACATCT
CGGGCATCGGCTTATACGCCAGAACCCTCGTCGGCGAAGAAGGTTCCCTCA
ATGTAGTCCATCAGGCCGAACCTCTCGAGGGGGGGCCGGTACCCAATTC
GCCCTATAGTGAGTCGATTACAATTCAGTGGCCGTCGTTTACAACGTCG
TGA CTGGGAAAACCTGGCGTTACCCAACCTAAGTCGCTTTGCAGCACAT
CCCC

FIG. 4 (cont.)

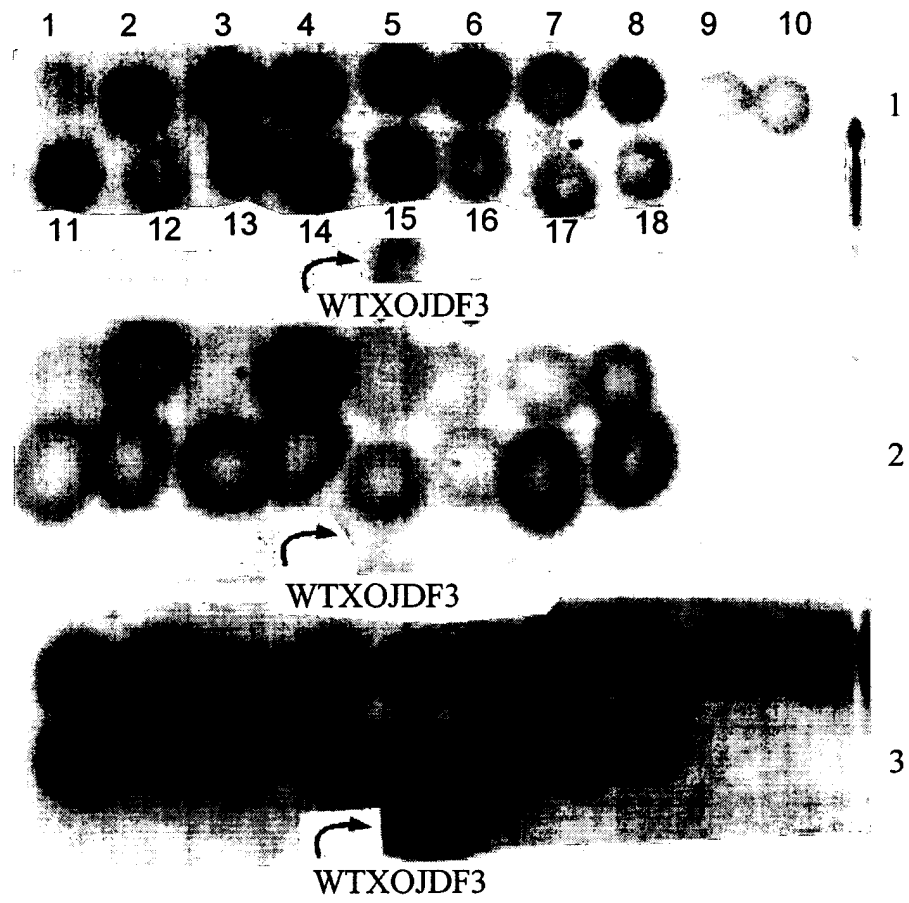


FIG. 5

Sequencing with Purified Mutants

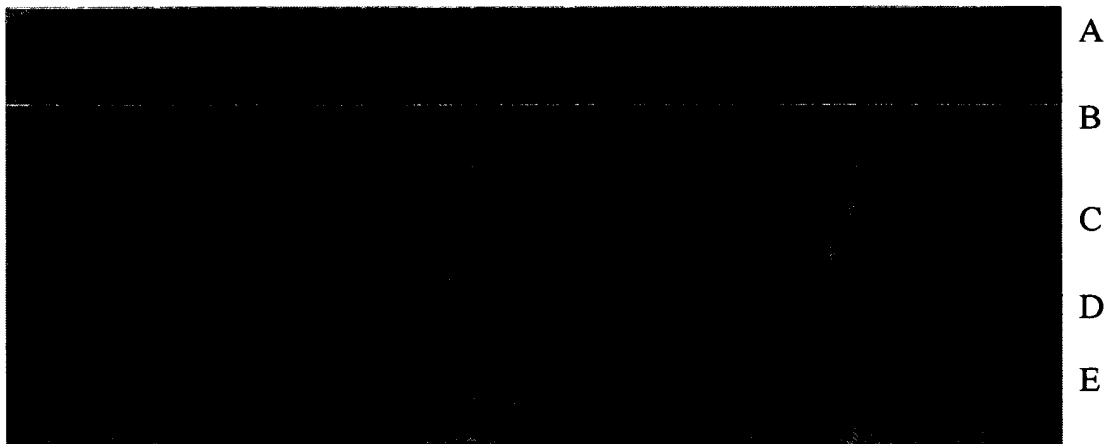


FIG. 6

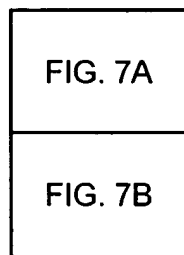
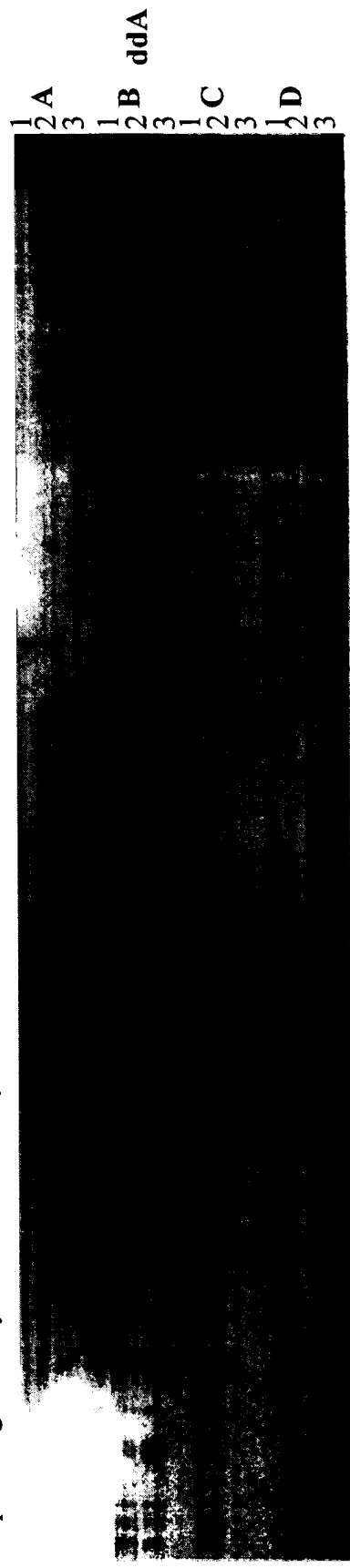


FIG. 7

Sequencing with Dye-labeled Dideoxynucleotides



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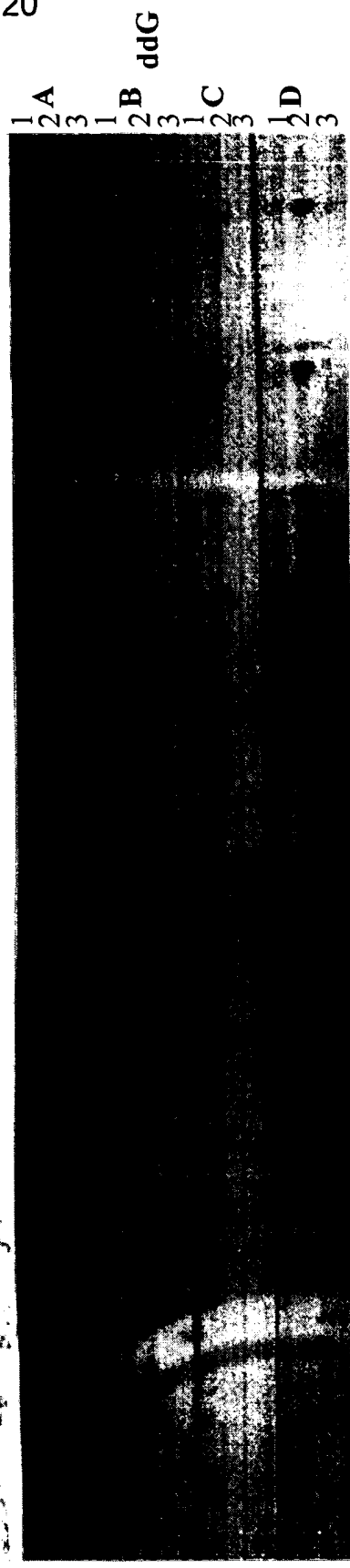
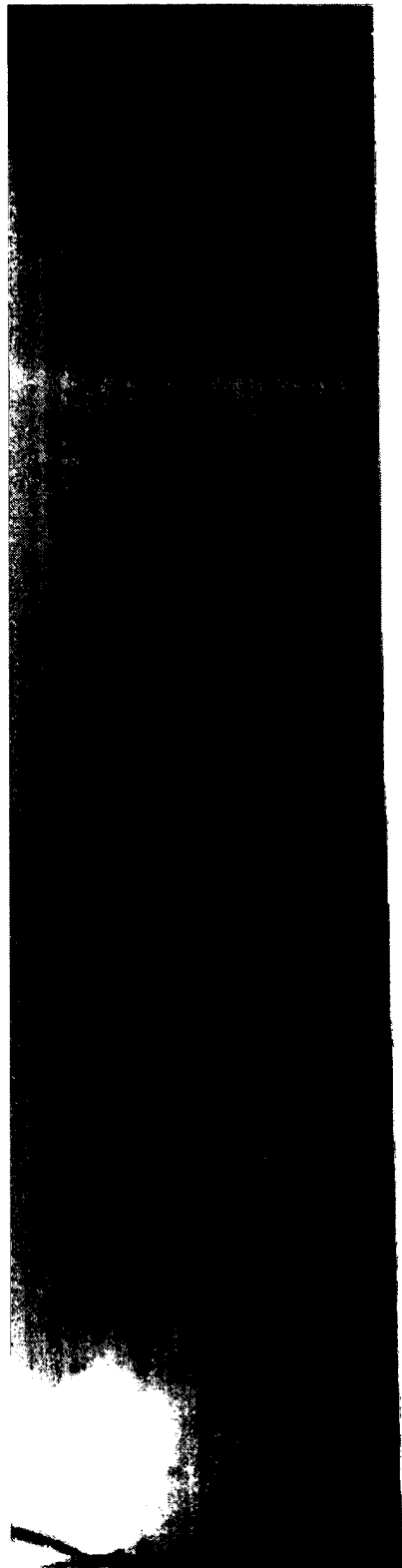


FIG. 7A

1A
2
3
1B ddC
2
3
1C
2
3
1D
2
3



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1A
2
3
1B ddT
2
3
1C
2
3
1D
2
3

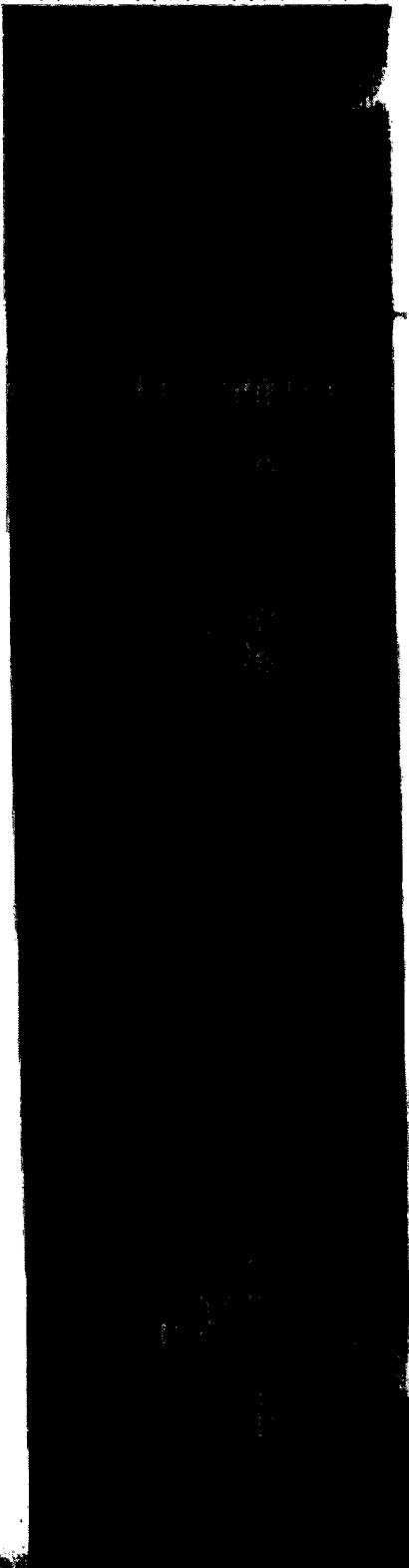


FIG. 7B

Sequencing with the P410L, A485T Double Mutant and α - 33 P Dideoxynucleotides



FIG. 8

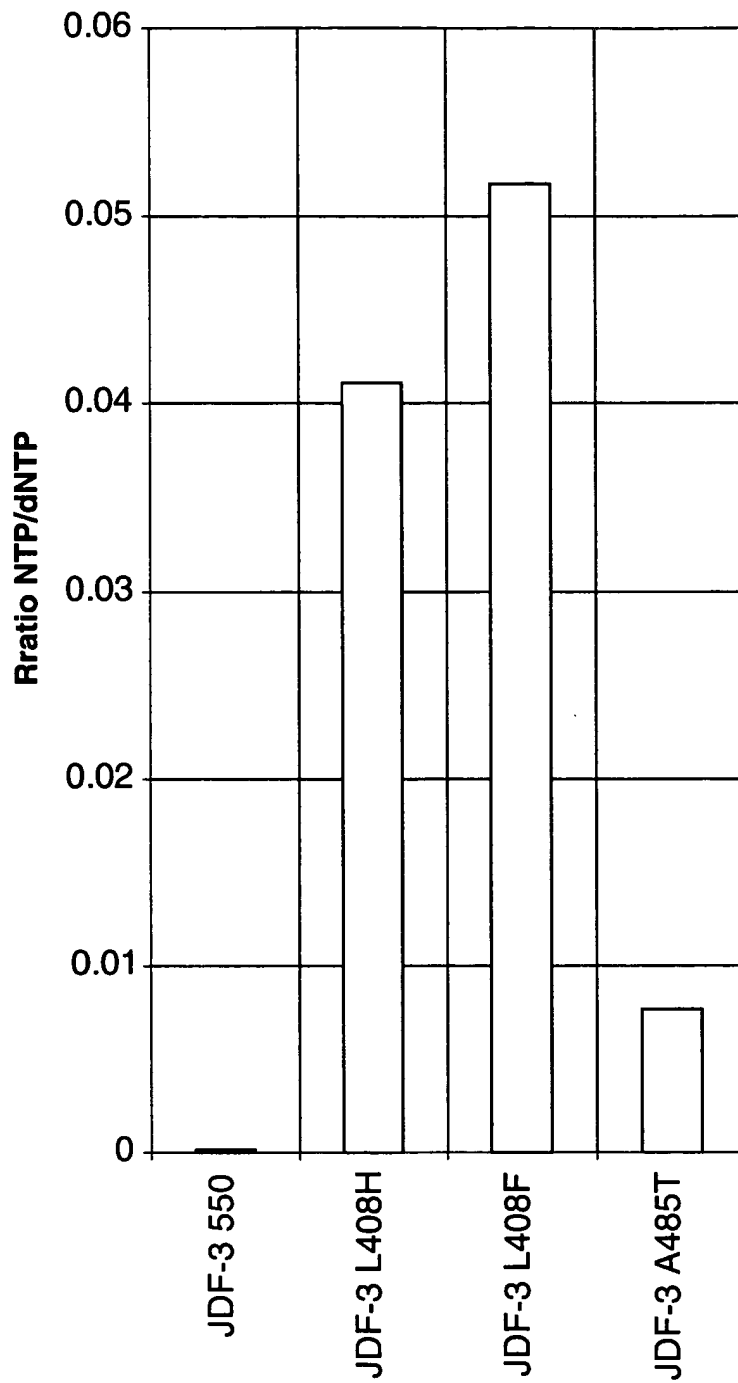


FIG. 9

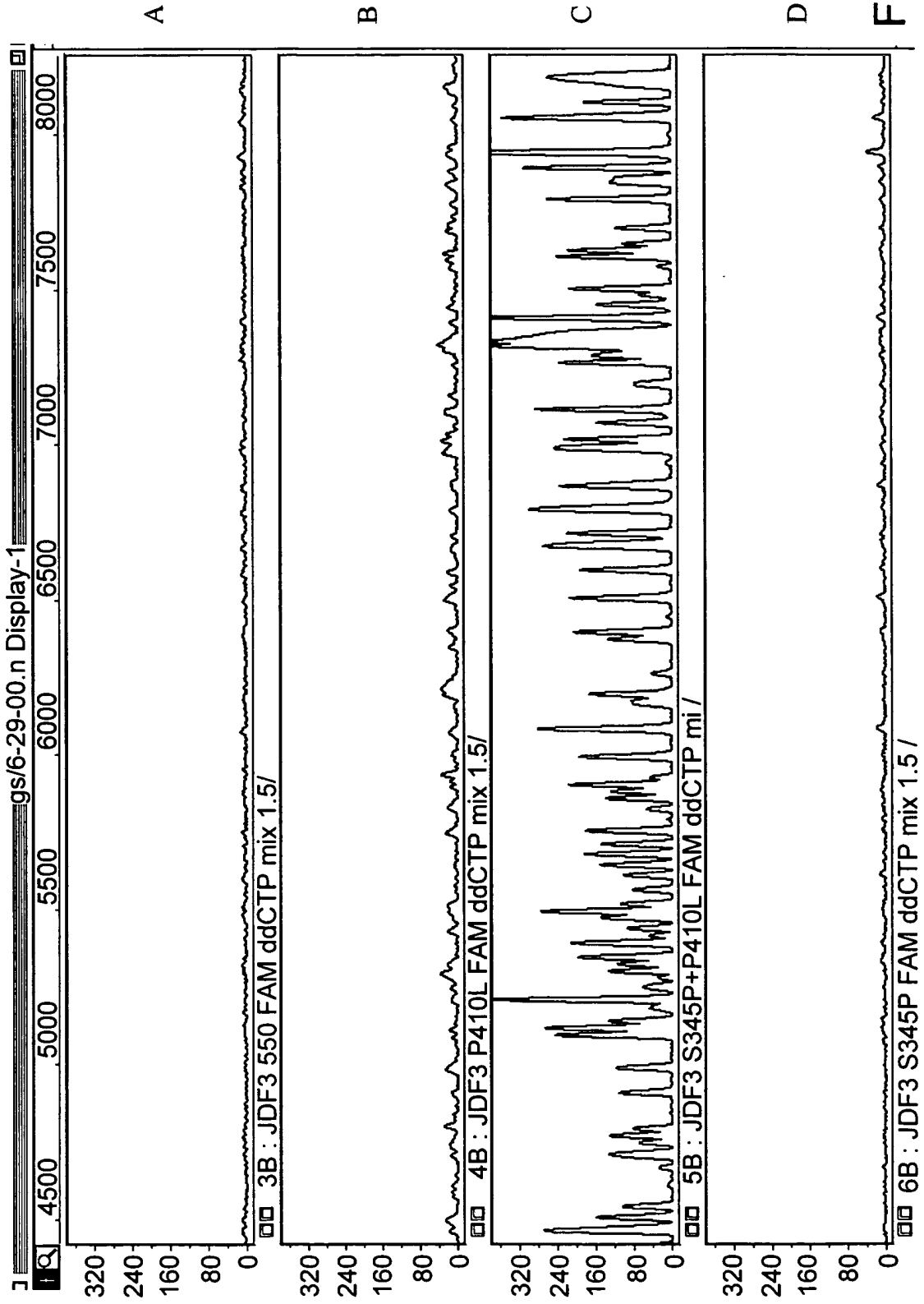


FIG. 10

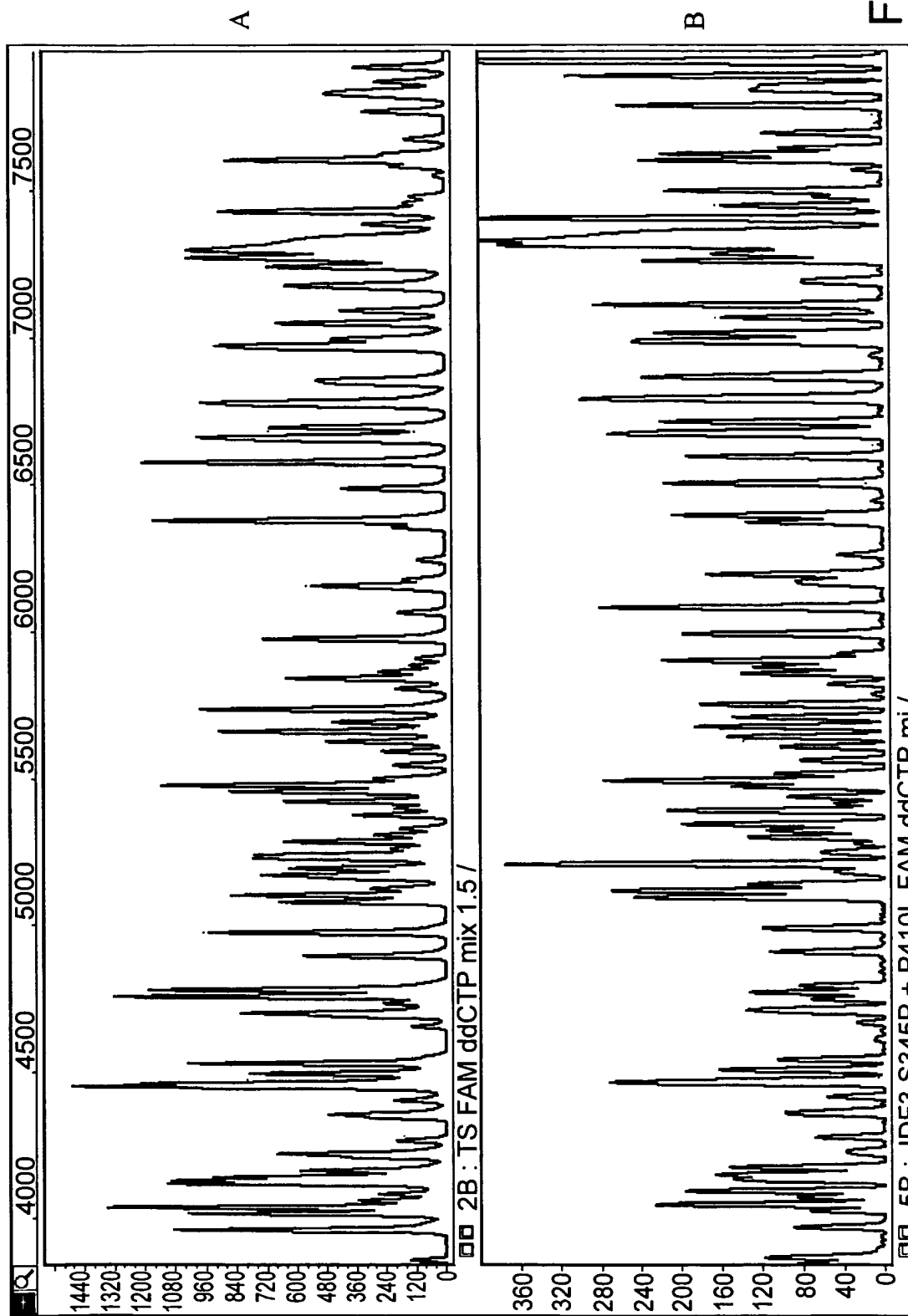


FIG. 11

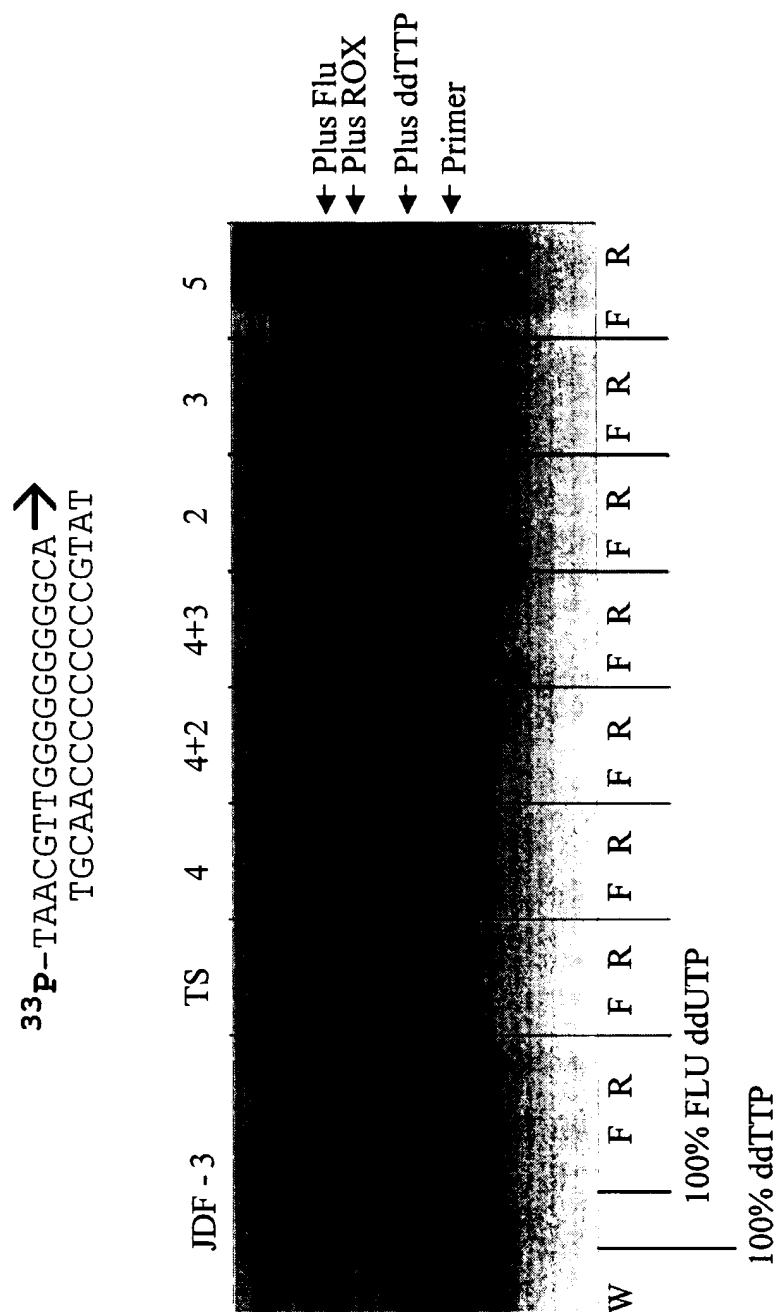
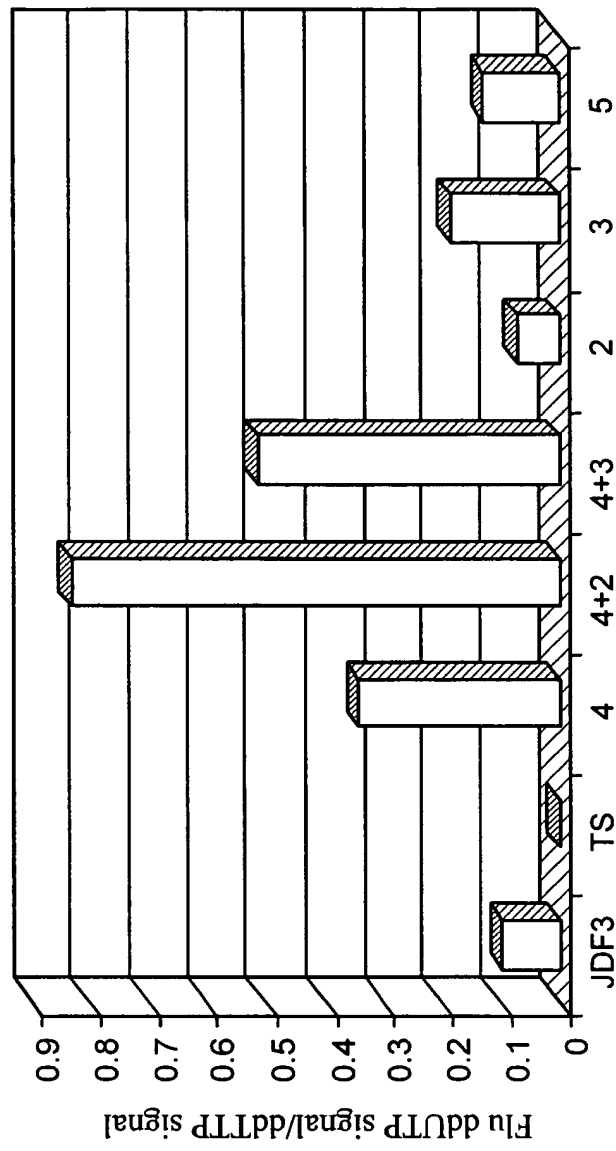


FIG. 12



Mutants

FIG. 13

4	1	-----LVXNAXSTGNLVEWFLLRK
10	1	-----VWDVSRSTGNLVERFLLRK
13	1	-----VWDVSRSTGNLVEWFLLRK
16	1	-----VWDVSRSTGNLVEWFLLRK
18	1	-----VWDVSRSTGNLVEWFLLRK
19	1	-----VWDVXRSTGNLVEWFLLRK
28	1	-----VWDVPRSTGNLVEWFLLRK
34	1	-----VWDVSRSTGNLVEWFLLRK
41	1	-----VWDVSRSTGNLVEWFLLRK
33	1	-----VWDVSRSTGNLVEWFLLRK
48	1	-----YWSXPXLRTGNLVEWFLLRK
55	1	-----VLGTXPSTGNLVEWFLLRK
64	1	-----XXXFWDVSRSTGNLVEWFLLRK
Jdf3	301	TGGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRK
		310 320 330 340 350 360
4	20	AYERNELAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
10	21	AYERNELAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHSVSP
13	21	AYERNELAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
16	21	AYERNELAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
18	21	AYERNELAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
19	21	AYERNELAPNKPDERELARRGGYAGGYVKEPERGQWDNIA_YLDFRSLYPSIIITHNVSP
28	21	AYERNELAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
34	21	AYERNELAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
41	21	AYERNELAPNKPDERELARRGGYAGGYVKEPERGPWDNIVYLDFRSLYPSIIITHNVSP
33	21	AYERNKLAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
48	21	AYERNELAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
55	22	AYERNELAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSHYPSIIITHNVSP
64	24	AYERNELAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
Jdf3	361	AYERNELAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSP
		370 380 390 400 410 420

FIG. 14

4 80 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴³⁰KATLDPLEKNLLD
 10 81 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴⁴⁰KATLDPLEKNLLD
 13 81 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴⁵⁰KATLDPLEKNLLD
 16 81 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴⁶⁰KATLDPLEKNLLD
 18 81 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴⁷⁰KATLDPLEKNLLD
 19 81 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴⁸⁰KATLDPLEKNLLD
 28 81 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴³⁰KATLDPLEKNLLD
 34 81 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴⁴⁰KATLDPLEKNLLD
 41 81 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴⁵⁰KATLDPLEKNLLD
 33 81 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴⁶⁰KATLDPLEKNLLD
 48 81 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴⁷⁰KATLDPLEKNLLD
 55 82 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴⁸⁰KATLDPLEKNLLD
 64 84 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴³⁰KATLDPLEKNLLD
 Jdf3 421 DTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLGNNLEERQKIKRKM⁴⁴⁰KATLDPLEKNLLD
 430 440 450 460 470 480

FIG. 14 (cont.)

4 140 YRQRAIKILANSYYGYCGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 10 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 13 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 16 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 18 141 YRQRAIKILANYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 19 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 28 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 34 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 41 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 33 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 48 141 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 55 142 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 64 144 YRQRAIKILANSYYGNYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD
 Jdf3 481 YRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYAD

490 500

4 200 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE
 10 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE
 13 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE
 16 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELKYEGFYVRGFFVTKKKYAVIDEE
 18 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE
 19 201 TDGLHATIPGADAETVKKKAMEFLNYINLKLPGLELEYEGFYVRGFFVTKKKXAVIDEE
 28 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE
 34 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE
 41 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE
 33 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLEPEYEGFYVRGFFVTKKKYAVIDEE
 48 201 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE
 55 202 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE
 64 204 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE
 Jdf3 541 TDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEE

550 560 570 580 590 600

FIG. 15

4 260 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL
 10 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEEL
 13 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVRKVTEKLSKYEVPPPEKL
 16 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL
 18 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHDDVEEAVRIVREVTEKLSKYEVPPPEKL
 19 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAIRIVREVTEKLSKYEVPPPEKL
 28 261 GKIATRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL
 34 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLNKYEVPPPEKL
 41 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL
 33 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL
 48 261 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPVKL
 55 262 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPGEA
 64 264 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL
 Jdf3 601 GKITTRGLEIVRRDWSEIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPPEKL
 610 620 630 640 650 660

FIG. 15 (cont.)

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